

SEQUENZPROTOKOLL

<110> Jomaa, Hassan

<120> Verfahren zur Identifizierung chemischer Wirkstoffe und
Wirkstoffe zur Hemmung des
1-Desoxy-D-xylulose-5-Phosphat-Biosynthesewegs

<130> 15514

<140> PCT/EP99/02463

<141> 1999-04-13

<150> DE19843279.3

<151> 1998-09-22

<150> DE19816196.4

<151> 1998-04-14

<150> DE19828097.1

<151> 1998-06-24

<150> DE19825585.3

<151> 1998-06-09

<150> DE19831637.2

<151> 1998-07-15

<150> DE19831639.3

<151> 1998-07-15

<150> DE19831638.0

<151> 1998-07-15

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 1467

<212> DNA

<213> Plasmodium falciparum

<220>

<221> CDS

<222> (1)..(1467)

<220>

<221> gene

<222> (1)..(1467)

<220>

<221> mRNA

<222> (1)..(1467)

<400> 1

atg aag aaa tat att tat ata tat ttt ttc ttc atc aca ata act att 48
Met Lys Lys Tyr Ile Tyr Phe Phe Ile Thr Ile Thr Ile
1 5 10 15

aat gat tta gta ata aat aat aca tca aaa tgt gtt tcc att gaa aga 96
Asn Asp Leu Val Ile Asn Asn Thr Ser Lys Cys Val Ser Ile Glu Arg
20 25 30

aga aaa aat aac gca tat ata aat tat ggt ata gga tat aat gga cca 144
Arg Lys Asn Asn Ala Tyr Ile Asn Tyr Gly Ile Gly Tyr Asn Gly Pro
35 40 45

gat aat aaaa at aca aag aat aga aga tgt aaa aga ata aag tta tgc 192
Asp Asn Lys Ile Thr Lys Ser Arg Arg Cys Lys Arg Ile Lys Leu Cys
50 55 60

aaa aag gat tta ata gat att ggt gca ata aag aaa cca att aat gta 240
Lys Lys Asp Leu Ile Asp Ile Gly Ala Ile Lys Lys Pro Ile Asn Val
65 70 75 80

gca att ttt gga aat act ggt agt ata ggt acg aat gct tta aat ata 288
Ala Ile Phe Gly Ser Thr Gly Ser Ile Gly Thr Asn Ala Leu Asn Ile
85 90 95

ata agg gag tgt aat aaa att gaa aat gtt ttt aat gtt aaa gca ttg 336
Ile Arg Glu Cys Asn Lys Ile Glu Asn Val Phe Asn Val Lys Ala Leu
100 105 110

tat gtg aat aag aat gtg aat gaa tta tat gaa caa gct aga gaa ttt 384
Tyr Val Asn Lys Ser Val Asn Glu Leu Tyr Glu Gln Ala Arg Glu Phe
115 120 125

tta cca gaa tat ttg tgt ata cat gat aaa aat gta tat gaa gaa tta 432
Leu Pro Glu Tyr Leu Cys Ile His Asp Lys Ser Val Tyr Glu Glu Leu
130 135 140

aaa gaa ctg gta aaa aat ata aaa gat tat aaa cct ata ata ttg tgt 480
Lys Glu Leu Val Lys Asn Ile Lys Asp Tyr Lys Pro Ile Ile Leu Cys
145 150 155 160

ggt gat gaa ggg atg aaa gaa ata tgt a.. agt aat agt ata gat aaa Gly Asp Glu Gly Met Lys Glu Ile Cys Ser Ser Asn Ser Ile Asp Lys	165	170	175	528	
ata gtt att ggt att gat tct ttt caa gga tta tat tct act atg tat Ile Val Ile Gly Ile Asp Ser Phe Gln Gly Leu Tyr Ser Thr Met Tyr	180	185	190	576	
gca att atg aat aat aaa ata gtt gcg tta gct aat aaa gaa tcc att Ala Ile Met Asn Asn Lys Ile Val Ala Leu Ala Asn Lys Glu Ser Ile	195	200	205	624	
gtc tct gct ggt ttc ttt tta aag aaa tta tta aat att cat aaa aat Val Ser Ala Gly Phe Phe Ile Lys Lys Leu Leu Asn Ile His Lys Asn	210	215	220	672	
gca aag ata ata cct gtt gat tca gaa cat agt gct ata ttt caa tgt Ala Lys Ile Ile Pro Val Asp Ser Glu His Ser Ala Ile Phe Gln Cys	225	230	235	240	720
tta gat aat aat aag gta tta aaa aca aaa tgt tta caa gac aat ttt Leu Asp Asn Asn Lys Val Ile Lys Thr Lys Cys Leu Gln Asp Asn Phe	245	250	255	768	
tct aaa att aac aat ata aat aaa ata ttt tta tgt tca tct gga ggt Ser Lys Ile Asn Asn Ile Asn Lys Ile Phe Leu Cys Ser Ser Gly Gly	260	265	270	816	
cca ttt caa aat tta act atg gac gaa tta aaa aat gta aca tca gaa Pro Phe Gln Asn Ile Thr Met Asp Glu Leu Lys Asn Val Thr Ser Glu	275	280	285	864	
aat gct tta aag cat cct aaa tgg aaa atg ggt aag aaa ata act ata Asn Ala Leu Lys His Pro Lys Trp Lys Met Gly Lys Ile Thr Ile	290	295	300	912	
gat tct gca act atg atg aat aaa ggt tta gag gtt ata gaa acc cat Asp Ser Ala Thr Met Met Asn Lys Gly Leu Glu Val Ile Glu Thr His	305	310	315	320	960
ttt tta ttt gat gta gat tat aat gat ata gaa gtt ata gta cat aaa Phe Leu Phe Asp Val Asp Tyr Asn Asp Ile Glu Val Ile Val His Lys	325	330	335	1008	
gaa tgc att ata cat tct tgt gtt gaa ttt ata gac aaa tca gta ata Glu Cys Ile Ile His Ser Cys Val Glu Phe Ile Asp Lys Ser Val Ile	340	345	350	1056	

agt caa atg tat tat cca gat atg caa ata ccc ata tta tat tct tta 1104
Ser Gln Met Tyr Tyr Pro Asp Met Gln Ile Pro Ile Leu Tyr Ser Leu
355 360 365

aca tgg cct gat aga ata aaa aca aat tta aaa cct tta gat ttg gct 1152
Thr Trp Pro Asp Arg Ile Lys Thr Asn Leu Lys Pro Leu Asp Leu Ala
370 375 380

cag gtt tca act ctt aca ttt cat aaa cct tct tta gaa cat ttc ccg 1200
Gln Val Ser Thr Leu Thr Phe His Lys Pro Ser Leu Glu His Phe Pro
385 390 395 400

tgt att aaa tta gct tat caa gca ggt ata aaa gga aac ttt tat cca 1248
Cys Ile Lys Leu Ala Tyr Gln Ala Gly Ile Lys Gly Asn Phe Tyr Pro
405 410 415

act gta sta aat gcg tca aat gaa ata gct aac aac tta ttt ttg aat 1296
Thr Val Leu Asn Ala Ser Asn Glu Ile Ala Asn Asn Leu Phe Leu Asn
420 425 430

aat aaa att aaa tat ttt gat att tcc tct ata ata tcg caa gtt ctt 1344
Asn Lys Ile Lys Tyr Phe Asp Ile Ser Ser Ile Ile Ser Gln Val Leu
435 440 445

gaa tct ttc aat tct caa aag gtt tcg gaa aat agt gaa gat tta atg 1392
Glu Ser Phe Asn Ser Gln Lys Val Ser Glu Asn Ser Glu Asp Leu Met
450 455 460

aag caa att cta caa ata cat tct tgg gcc aaa gat aaa gct acc gat 1440
Lys Gln Ile Leu Gln Ile His Ser Trp Ala Lys Asp Lys Ala Thr Asp
465 470 475 480

ata tac aac aaa cat aat tct tca tag 1467
Ile Tyr Asn Lys His Asn Ser Ser
485

<210> 2

<211> 438

<212> PRT

<213> Plasmodium falciparum

<400> 2
Met Lys Lys Tyr Ile Tyr Ile Tyr Phe Phe Phe Ile Thr Ile Thr Ile
1 5 10 15

Asn Asp Leu Val Ile Asn Asn Thr Ser Lys Cys Val Ser Ile Glu Arg
20 25 30

Arg Lys Asn Asn Ala Tyr Ile Asn Tyr Gly Ile Gly Tyr Asn Gly Pro
35 40 45

Asp Asn Lys Ile Thr Lys Ser Arg Arg Cys Lys Arg Ile Lys Leu Cys
50 55 60

Lys Lys Asp Leu Ile Asp Ile Gly Ala Ile Lys Lys Pro Ile Asn Val
65 70 75 80

Ala Ile Phe Gly Ser Thr Gly Ser Ile Gly Thr Asn Ala Leu Asn Ile
85 90 95

Ile Arg Glu Cys Asn Lys Ile Glu Asn Val Phe Asn Val Lys Ala Leu
100 105 110

Tyr Val Asn Lys Ser Val Asn Glu Leu Tyr Glu Gln Ala Arg Glu Phe
115 120 125

Ieu Pro Glu Tyr Ieu Cys Ile His Asp Lys Ser Val Tyr Glu Glu Leu
130 135 140

Lys Glu Leu Val Lys Asn Ile Lys Asp Tyr Lys Pro Ile Ile Leu Cys
145 150 155 160

Gly Asp Glu Gly Met Lys Glu Ile Cys Ser Ser Asn Ser Ile Asp Lys
165 170 175

Ile Val Ile Gly Ile Asp Ser Phe Gln Gly Leu Tyr Ser Thr Met Tyr
180 185 190

Ala Ile Met Asn Asn Lys Ile Val Ala Leu Ala Asn Lys Glu Ser Ile
195 200 205

Val Ser Ala Gly Phe Phe Leu Lys Leu Leu Asn Ile His Lys Asn
210 215 220

Ala Lys Ile Ile Pro Val Asp Ser Glu His Ser Ala Ile Phe Gln Cys
225 230 235 240

Leu Asp Asn Asn Lys Val Leu Lys Thr Lys Cys Leu Gln Asp Asn Phe
245 250 255

Ser Lys Ile Asn Asn Ile Asn Lys Ile Phe Leu Cys Ser Ser Gly Gly
260 265 270

Pro Phe Gln Asn Ieu Thr Met Asp Glu Leu Lys Asn Val Thr Ser Glu
275 280 285

Asn Ala Leu Lys His Pro Lys Trp Lys Met Gly Lys Lys Ile Thr Ile
290 295 300

Asp Ser Ala Thr Met Met Asn Lys Gly Leu Glu Val Ile Glu Thr His
305 310 315 320

Phe Leu Phe Asp Val Asp Tyr Asn Asp Ile Glu Val Ile Val His Lys
325 330 335

Glu Cys Ile Ile His Ser Cys Val Glu Phe Ile Asp Lys Ser Val Ile
340 345 350

Ser Gln Met Tyr Tyr Pro Asp Met Gln Ile Pro Ile Leu Tyr Ser Leu
355 360 365

Thr Trp Pro Asp Arg Ile Lys Thr Asn Leu Lys Pro Leu Asp Leu Ala
370 375 380

Gln Val Ser Thr Leu Thr Phe His Lys Pro Ser Leu Glu His Phe Pro
385 390 395 400

Cys Ile Lys Leu Ala Tyr Gln Ala Gly Ile Lys Gly Asn Phe Tyr Pro
405 410 415

Thr Val Leu Asn Ala Ser Asn Glu Ile Ala Asn Asn Leu Phe Leu Asn
420 425 430

Asn Lys Ile Lys Tyr Phe Asp Ile Ser Ser Ile Ile Ser Gln Val Leu
435 440 445

Glu Ser Phe Asn Ser Gln Lys Val Ser Glu Asn Ser Glu Asp Leu Met
450 455 460

Lys Gln Ile Leu Gln Ile His Ser Trp Ala Lys Asp Lys Ala Thr Asp
465 470 475 480

Ile Tyr Asn Lys His Asn Ser Ser
485

<210> 3
<211> 3872
<212> DNA
<213> Plasmodium falciparum

<220>

<221> CDS

<222> (126)..(3740)

<220>

<221> gene

<222> (1)..(3870)

<220>

<221> mRNA

<222> (1)..(3870)

<400> 3

ggtaatata: gtataatata taataatata attcttacgt atgtatcatt tatgaatcat 60

aataatattc taaatttacc tttttttttt gtcgatctt ctcattttcg tttagcttt 120

tatca atg att ttt aat tat gtg ttt ttt aag aac ttt gta cca gtt gtt 170

Met Ile Phe Asn Tyr Val Phe Phe Lys Asn Phe Val Pro Val Val

1 5 10 15

cta tac att ctc ctt ata ata tat att aac tta aat ggc atg aat aat 218

Leu Tyr Ile Leu Leu Ile Tyr Ile Asn Leu Asn Gly Met Asn Asn

20 25 30

aaa aat caa ata aaa aca gaa aaa att tat ata aag aaa ttg aat agg 266

Lys Asn Gln Ile Lys Thr Glu Lys Ile Tyr Ile Lys Lys Leu Asn Arg

35 40 45

ttg tca agg aaa aat tcg tta tgt agt tct aaa aat aaa ata gca tgc 314

Leu Ser Arg Lys Asn Ser Ile Cys Ser Ser Lys Asn Lys Ile Ala Cys

50 55 60

ttg ttc gat ata gga aat gat gat aat aga aat acg aca tat ggc tat 362

Leu Phe Asp Ile Gly Asn Asp Asp Asn Arg Asn Thr Thr Tyr Gly Tyr

65 70 75

aat gtg aat gtt aaa aat gat gat att aat tcc tta cta aaa aat aat 410

Asn Val Asn Val Lys Asn Asp Asp Ile Asn Ser Leu Leu Lys Asn Asn

80 85 90 95

tat agt aat aaa ttg tac atg gat aag agg aaa aat att aat aat gta 458

Tyr Ser Asn Lys Ile Tyr Met Asp Lys Arg Lys Asn Ile Asn Asn Val

100 105 110

att agt act aat aaa ata tct ggg tcc att tca aat att tgt agt aga 506

Ile Ser Thr Asn Lys Ile Ser Gly Ser Ile Ser Asn Ile Cys Ser Arg

115 120 125

aat caa aaa gaa aat gaa cca aaa aga aat aaa caa aga tgc tta act		554	
Asn Gln Lys Glu Asn Glu Gln Lys Arg Asn Lys Gln Arg Cys Leu Thr			
130	135	140	
caa tgt cac act tat aat atg tca cat gaa cag gac aaa cta gct aat		602	
Gln Cys His Thr Tyr Asn Met Ser His Glu Gln Asp Lys Leu Ala Asn			
145	150	155	
gat aat aat agg aat aat aca aag aat ttt aat tta tta ttt ata aat		650	
Asp Asn Asn Arg Asn Asn Lys Lys Asn Phe Asn Leu Leu Phe Ile Asn			
160	165	170	175
tat ttt aat ttg aaa cga atg aaa aat tct ctt cta aat aaa gac aat		698	
Tyr Phe Asn Leu Lys Arg Met Lys Asn Ser Leu Leu Asn Lys Asp Asn			
180	185	190	
ttc ttt tac tgt aaa gaa aca aaa ttg tca ttt ctg cat aag gcc tat		746	
Phe Phe Tyr Cys Lys Glu Lys Leu Ser Phe Leu His Lys Ala Tyr			
195	200	205	
aaa aaa aaa aat tgc act ttt caa aat tat agt tta aca aga aca tct		794	
Lys Lys Asn Cys Thr Phe Gln Asn Tyr Ser Leu Lys Arg Lys Ser			
210	215	220	
aat cgt gat tca cat aca ttt ttt tct gga gaa ttt gac gat tat aca		842	
Asn Arg Asp Ser His Lys Leu Phe Ser Gly Glu Phe Asp Asp Tyr Thr			
225	230	235	
aat aat aat gct tta tat gaa tcc gaa aca aat gaa tac att aca cta		890	
Asn Asn Asn Ala Leu Tyr Glu Ser Glu Lys Lys Glu Tyr Ile Thr Leu			
240	245	250	255
aat		938	
Asn Asn Asn Asn Lys Asn Asn Asn Lys Asn Asn Asn Asp Asn Lys Asn			
260	265	270	
aat gat aat aat gat tat aat aat aat aat aat aat aat aat tta gga		986	
Asn Asp Asn Asn Asp Tyr Asn Asn Asn Ser Cys Asn Asn Leu Gly			
275	280	285	
gag aga tcc aat cat tat gat aat tat ggt gga gat aat aat aat cca		1034	
Glu Arg Ser Asn His Tyr Asp Asn Tyr Gly Gly Asp Asn Asn Asn Pro			
290	295	300	
tgt aat aat aat aat gac aca tat gat atg gga aca tat ttc aca cag		1082	
Cys Asn Asn Asn Asn Asp Lys Tyr Asp Ile Gly Lys Tyr Phe Lys Gln			
305	310	315	

att aat acc ttt att aat att gat gaa tat aaa act ata tat ggt gat Ile Asn Thr Phe Ile Asn Ile Asp Glu Tyr Lys Thr Ile Tyr Gly Asp 320 325 330 335	1130
gaa ata tat aaa gaa ata tat gaa cta tat gta gaa aga aat att cct Glu Ile Tyr Lys Glu Ile Tyr Glu Leu Tyr Val Glu Arg Asn Ile Pro 340 345 350	1173
gaa tat tat gaa cga aaa tat ttt tca gaa gat att aaa aag agt gtc Glu Tyr Tyr Glu Arg Lys Tyr Phe Ser Glu Asp Ile Lys Ser Val 355 360 365	1226
cta ttt gat ata gat aaa tat aat gat gtc gaa ttt gaa aaa gct ata Ile Phe Asp Ile Asp Lys Tyr Asn Asp Val Glu Phe Glu Lys Ala Ile 370 375 380	1274
aaa gaa gaa ttt ata aat aat gga gtt tat att aat aat ata gat aat Lys Glu Glu Phe Ile Asn Asn Gly Val Tyr Ile Asn Asn Ile Asp Asn 385 390 395	1322
aca tat tat aaa gaa aat att tta ata atg aaa aag ata tta cat Thr Tyr Tyr Lys Glu Asn Ile Leu Ile Met Lys Lys Ile Leu His 400 405 410 415	1370
tat ttc cca tta tta aaa tta att aat aat cca tca gat tta aaa aag Tyr Phe Pro Leu Ile Lys Ile Asn Asn Pro Ser Asp Leu Lys Lys 420 425 430	1418
tta aaa aaa caa tat tta cct tta tta gca cat gaa tta aaa ata ttt Leu Lys Lys Gln Tyr Leu Pro Leu Leu Ala His Glu Leu Lys Ile Phe 435 440 445	1466
tta ttt ttt att gta aat aat aca gga ggt cat ttt tcc tct gtt tta Leu Phe Phe Ile Val Asn Ile Thr Gly Gly His Phe Ser Ser Val Leu 450 455 460	1514
agc tct tta gaa att caa tta tta ttg tat att ttt aat caa cca Ser Ser Leu Glu Ile Gln Leu Leu Leu Tyr Ile Phe Asn Gln Pro 465 470 475	1562
tat gat aat gtt ata tat gat ata gga cat caa gca tat gta cat aag Tyr Asp Asn Val Ile Tyr Asp Ile Gly His Gln Ala Tyr Val His Lys 480 485 490 495	1610
ata ttg acc gga aga aaa cta tta ttt cta tca tta aga aat aaa aaa Ile Leu Thr Gly Arg Lys Leu Leu Phe Leu Ser Leu Arg Asn Lys Lys 500 505 510	1658

ggt att agt gga ttc cta aat att ttt gaa agt att tat gat aaa ttt Gly Ile Ser Gly Phe Leu Asn Ile Phe Glu Ser Ile Tyr Asp Lys Phe	515	520	525	1706	
ggg gct ggt cac agt tcc act tca tta agt gct ata caa gga tat tat Gly Ala Gly His Ser Ser Thr Ser Leu Ser Ala Ile Gln Gly Tyr Tyr	530	535	540	1754	
gaa ggc gag tgg caa gtg aag aat aaa gaa aaa tat gga aat gga gat Glu Ala Glu Trp Gln Val Lys Asn Lys Glu Lys Tyr Gly Asn Gly Asp	545	550	555	1802	
ata gaa ata agt gat aac gca aat gtc acg aat aat gaa agg ata ttt Ile Glu Ile Ser Asp Asn Ala Asn Val Thr Asn Asn Glu Arg Ile Phe	560	565	570	575	1850
caa aaa gga ata cac aat gat aat aat att aac aat aat att aat aat Gln Lys Gly Ile His Asn Asp Asn Asn Ile Asn Asn Asn Ile Asn Asn	580	585	590	1898	
aat aat tat atc aat cct tca gat gtg gta gga aga gaa aat acg aat Asn Asn Tyr Ile Asn Pro Ser Asp Val Val Gly Arg Glu Asn Thr Asn	595	600	605	1946	
gta cca aat gta cga aat gat aac cat aac gtg gat aaa gta cac att Val Pro Asn Val Arg Asn Asp Asn His Asn Val Asp Lys Val His Ile	610	615	620	1994	
gct att ata gga gat ggt ggt tta aca ggt gga atg gca tta gaa gcg Ala Ile Ile Gly Asp Gly Gly Leu Thr Gly Gly Met Ala Leu Glu Ala	625	630	635	2042	
tta aat tat att tca ttc ttg aat tct aaa att tta att att tat aat Leu Asn Tyr Ile Ser Phe Leu Asn Ser Lys Ile Leu Ile Ile Tyr Asn	640	645	650	655	2090
gat aac gga caa gtt tct tta cca aca aat gcc gta agt ata tca ggt Asp Asn Gly Gln Val Ser Leu Pro Thr Asn Ala Val Ser Ile Ser Gly	660	665	670	2138	
aat aga cct ata ggt tct ata tca gat cat tta cat tat ttt gtt tct Asn Arg Pro Ile Gly Ser Ile Ser Asp His Leu His Tyr Phe Val Ser	675	680	685	2186	
aat ata gaa gca aat gct ggt gat aat aaa tta tcg aaa aat gca aaa Asn Ile Glu Ala Asn Ala Gly Asp Asn Lys Leu Ser Lys Asn Ala Lys	690	695	700	2234	

gag aat aac att ttt gaa aat ttg aat tat gat tat att ggt gtt gtg Glu Asn Asn Ile Phe Glu Asn Leu Asn Tyr Asp Tyr Ile Gly Val Val	705	710	715	2282	
aat ggt aat aat aca gaa gag ctc ttt aaa gta tta aat aat ata aaa Asn Gly Asn Asn Thr Glu Glu Leu Phe Lys Val Leu Asn Asn Ile Lys	720	725	730	735	2330
gaa aat aaa tta aaa aga gct act gtt ctt cat gta cgt aca aaa aaa Glu Asn Lys Leu Lys Arg Ala Thr Val Leu His Val Arg Thr Lys Lys	740	745	750	2378	
tcg aat gat ttt ata aat tca aag agt cca ata agt ata ttg cac tct Ser Asn Asp Phe Ile Asn Ser Lys Ser Pro Ile Ser Ile Leu His Ser	755	760	765	2426	
ata aag aaa aat gag att ttc cct ttc gat acc act ata tta aat gga Ile Lys Asn Glu Ile Phe Pro Phe Asp Thr Thr Ile Leu Asn Gly	770	775	780	2474	
aat att cat aag gag aac aag ata gaa gaa gag aaa aat gtt tct tca Asn Ile His Lys Glu Asn Lys Ile Glu Glu Lys Asn Val Ser Ser	785	790	795	2522	
tct aca aag tat gat gta aat aat aag aat aat aaa aat aat gat aat Ser Thr Lys Tyr Asp Val Asn Asn Lys Asn Asn Lys Asn Asp Asn	800	805	810	815	2570
agt gaa att ata aaa tat gaa gat atg ttt tca aaa gag acg ttc aca Ser Glu Ile Ile Lys Tyr Glu Asp Met Phe Ser Lys Glu Thr Phe Thr	820	825	830	2618	
gat ata tat aca aat gaa atg tta aaa tat tta aag aaa gat aga aat Asp Ile Tyr Thr Asn Glu Met Leu Lys Tyr Leu Lys Lys Asp Arg Asn	835	840	845	2666	
ata ata ttc cta tct ccc gct atg tta gga gga tca gga ttg gtt aaa Ile Ile Phe Leu Ser Pro Ala Met Leu Gly Gly Ser Gly Leu Val Lys	850	855	860	2714	
att agt gag cgt tat cca aat aat gta tat gat gta ggt ata gca gaa Ile Ser Glu Arg Tyr Pro Asn Asn Val Tyr Asp Val Gly Ile Ala Glu	865	870	875	2762	
caa cat tct gta act ttc gca gca gct atg gca atg aat aag aaa tta Gln His Ser Val Thr Phe Ala Ala Ala Met Ala Met Asn Lys Lys Leu	880	885	890	895	2810

aaa atc caa tta tgt ata tat tcg acc ttt tta caa aga gca tat gat Lys Ile Gln Leu Cys Ile Tyr Ser Thr Phe Leu Gin Arg Ala Tyr Asp	900	905	910	2858
caa att ata cat gat ctt aat tta caa aat ata cct tta aag gtt ata Gln Ile Ile His Asp Leu Asn Leu Gln Asn Ile Pro Leu Lys Val Ile	915	920	925	2906
att gga aga agt gga tta gta gga gag gat ggg gca aca cat caa ggt Ile Gly Arg Ser Gly Leu Val Gly Glu Asp Gly Ala Thr His Gln Gly	930	935	940	2954
ata tat gat tta tat tat ctt ggg aca ctt aac aat gca tat ata ata Ile Tyr Asp Leu Ser Tyr Leu Gly Thr Leu Asn Asn Ala Tyr Ile Ile	945	950	955	3002
tct cca agt aat caa gtt gat ttg aaa aga gct ctt agg ttt gct tat Ser Pro Ser Asn Gln Val Asp Leu Lys Arg Ala Leu Arg Phe Ala Tyr	960	965	970	3050
tta gat aag gac cat tct gtg tat ata cgt ata ccc aga atg aac ata Leu Asp Lys Asp His Ser Val Tyr Ile Arg Ile Pro Arg Met Asn Ile	980	985	990	3098
tta agt gat aag tac atg aaa gga tat ttg aac att cat atg aaa aat Leu Ser Asp Lys Tyr Met Lys Gly Tyr Leu Asn Ile His Met Lys Asn	995	1000	1005	3146
gag aac aaa aat atc gat gta aac gtg gat ata aac gat gat gta gat Glu Ser Lys Asn Ile Asp Val Asn Val Asp Ile Asn Asp Asp Val Asp	1010	1015	1020	3194
aaa tat agt gaa gaa tat atg gac gat gat aat ttt ata aaa tcg ttt Lys Tyr Ser Glu Glu Tyr Met Asp Asp Asn Phe Ile Lys Ser Phe	1025	1030	1035	3242
att gga aaa tct aga att att aaa atg gat aat gaa aat aat aat aca Ile Gly Lys Ser Arg Ile Ile Lys Met Asp Asn Glu Asn Asn Asn Thr	1040	1045	1050	3290
aat gaa cat tat tca agc aga gga gat aca cag aca aaa aaa aaa Asn Glu His Tyr Ser Ser Arg Gly Asp Thr Gln Thr Lys Lys Lys	1060	1065	1070	3338
gtt tgt atc ttt aac atg ggt agt atg ctt ttt aat gta att aat gct Val Cys Ile Phe Asn Met Gly Ser Met Leu Phe Asn Val Ile Asn Ala	1075	1080	1085	3386

ata aac gaa att gaa aaa gaa caa tat att tca cat aat tat tct ttt 3434
Ile Lys Glu Ile Glu Lys Glu Gln Tyr Ile Ser His Asn Tyr Ser Phe
1090 1095 1100

tca att gtt gat atg ata ttt tta aat cct tta gat aaa aat atg ata 3482
Ser Ile Val Asp Met Ile Phe Leu Asn Pro Leu Asp Lys Asn Met Ile
1105 1110 1115

gat cat gta ata aaa caa aat aaa cat caa tat tta att act tat gaa 3530
Asp His Val Ile Lys Gln Asn Lys His Gln Tyr Leu Ile Thr Tyr Glu
1120 1125 1130 1135

gat aat act ata ggt ggt ttt tct aca cat ttc aat aat tat tta ata 3578
Asp Asn Thr Ile Gly Gly Phe Ser Thr His Phe Asn Asn Tyr Leu Ile
1140 1145 1150

gaa aat aat tat att aca aaa cat aac tta tat gtt cat aat att tat 3626
Glu Asn Asn Tyr Ile Thr Lys His Asn Leu Tyr Val His Asn Ile Tyr
1155 1160 1165

tta tct aat gag cca att gaa cat gca tct ttt aag gat caa caa gaa 3674
Leu Ser Asn Glu Pro Ile Glu His Ala Ser Phe Lys Asp Gln Gln Glu
1170 1175 1180

gtc gtc aaa atg gat aaa tgt agt ctt gtc aat aga att aaa aat tat 3722
Val Val Lys Met Asp Lys Cys Ser Leu Val Asn Arg Ile Lys Asn Tyr
1185 1190 1195

ctt aac aat aat cct aca tcatgtaaaga taaatatata tttctaaaaat 3770
Leu Lys Asn Asn Pro Thr
1200 1205

tatatatat ttatacttta atgtgtacaa taaaatatat atctaaatat attttatttg 3830

tacgctttt tttttttt ttaattgtt attttggat at 3872

<210> 4
<211> 1205
<212> PRT
<213> Plasmodium falciparum

<400> 4
Met Ile Phe Asn Tyr Val Phe Phe Lys Asn Phe Val Pro Val Val Leu
1 5 10 15

Tyr Ile Leu Leu Ile Tyr Ile Asn Leu Asn Gly Met Asn Asn Lys
20 25 30

Asn Gln Ile Lys Thr Glu Lys Ile Tyr Ile Lys Lys Leu Asn Arg Leu
35 40 45

Ser Arg Lys Asn Ser Leu Cys Ser Ser Lys Asn Lys Ile Ala Cys Leu
50 55 60

Phe Asp Ile Gly Asn Asp Asp Asn Arg Asn Thr Thr Tyr Gly Tyr Asn
65 70 75 80

Val Asn Val Lys Asn Asp Asp Ile Asn Ser Leu Leu Lys Asn Asn Tyr
85 90 95

Ser Asn Lys Leu Tyr Met Asp Lys Arg Lys Asn Ile Asn Asn Val Ile
100 105 110

Ser Thr Asn Lys Ile Ser Gly Ser Ile Ser Asn Ile Cys Ser Arg Asn
115 120 125

Gln Lys Glu Asn Glu Gln Lys Arg Asn Lys Gln Arg Cys Leu Thr Gln
130 135 140

Cys His Thr Tyr Asn Met Ser His Glu Gln Asp Lys Leu Ala Asn Asp
145 150 155 160

Asn Asn Arg Asn Asn Lys Asn Phe Asn Leu Leu Phe Ile Asn Tyr
165 170 175

Phe Asn Leu Lys Arg Met Lys Asn Ser Leu Leu Asn Lys Asp Asn Phe
180 185 190

Phe Tyr Cys Lys Glu Lys Leu Ser Phe Leu His Lys Ala Tyr Lys
195 200 205

Lys Lys Asn Cys Thr Phe Gln Asn Tyr Ser Leu Lys Arg Lys Ser Asn
210 215 220

Arg Asp Ser His Lys Leu Phe Ser Gly Glu Phe Asp Asp Tyr Thr Asn
225 230 235 240

Asn Asn Ala Leu Tyr Glu Ser Glu Lys Lys Glu Tyr Ile Thr Leu Asn
245 250 255

Asn Asn Asn Lys Asn Asn Asn Lys Asn Asn Asp Asn Lys Asn Asn
260 265 270

Asp Asn Asn Asp Tyr Asn Asn Asn Ser Cys Asn Asn Leu Gly Glu
275 280 285

Arg Ser Asn His Tyr Asp Asn Tyr Gly Gly Asp Asn Asn Asn Pro Cys
290 295 300

Asn Asn Asn Asn Asp Lys Tyr Asp Ile Gly Lys Tyr Phe Lys Gln Ile
305 310 315 320

Asn Thr Phe Ile Asn Ile Asp Glu Tyr Lys Thr Ile Tyr Gly Asp Glu
325 330 335

Ile Tyr Lys Glu Ile Tyr Glu Leu Tyr Val Glu Arg Asn Ile Pro Glu
340 345 350

Tyr Tyr Glu Arg Lys Tyr Phe Ser Glu Asp Ile Lys Lys Ser Val Leu
355 360 365

Phe Asp Ile Asp Lys Tyr Asn Asp Val Glu Phe Glu Lys Ala Ile Lys
370 375 380

Glu Glu Phe Ile Asn Asn Gly Val Tyr Ile Asn Asn Ile Asp Asn Thr
385 390 395 400

Tyr Tyr Lys Lys Glu Asn Ile Leu Ile Met Lys Lys Ile Leu His Tyr
405 410 415

Phe Pro Leu Leu Lys Leu Ile Asn Asn Pro Ser Asp Leu Lys Lys Leu
420 425 430

Lys Lys Gln Tyr Leu Pro Leu Leu Ala His Glu Leu Lys Ile Phe Leu
435 440 445

Phe Phe Ile Val Asn Ile Thr Gly Gly His Phe Ser Ser Val Leu Ser
450 455 460

Ser Leu Glu Ile Gln Leu Leu Leu Tyr Ile Phe Asn Gln Pro Tyr
465 470 475 480

Asp Asn Val Ile Tyr Asp Ile Gly His Gln Ala Tyr Val His Lys Ile
485 490 495

Leu Thr Gly Arg Lys Leu Leu Phe Leu Ser Leu Arg Asn Lys Lys Gly
500 505 510

Ile Ser Gly Phe Leu Asn Ile Phe Glu Ser Ile Tyr Asp Lys Phe Gly
515 520 525

Ala Gly His Ser Ser Thr Ser Leu Ser Ala Ile Gln Gly Tyr Tyr Glu
530 535 540

Ala Glu Trp Gln Val Lys Asn Lys Glu Lys Tyr Gly Asn Gly Asp Ile
545 550 555 560

Glu Ile Ser Asp Asn Ala Asn Val Thr Asn Asn Glu Arg Ile Phe Gln
565 570 575

Lys Gly Ile His Asn Asp Asn Asn Ile Asn Asn Asn Ile Asn Asn Asn
580 585 590

Asn Tyr Ile Asn Pro Ser Asp Val Val Gly Arg Glu Asn Thr Asn Val
595 600 605

Pro Asn Val Arg Asn Asp Asn His Asn Val Asp Lys Val His Ile Ala
610 615 620

Ile Ile Gly Asp Gly Gly Leu Thr Gly Gly Met Ala Leu Glu Ala Leu
625 630 635 640

Asn Tyr Ile Ser Phe Leu Asn Ser Lys Ile Leu Ile Ile Tyr Asn Asp
645 650 655

Asn Gly Gln Val Ser Leu Pro Thr Asn Ala Val Ser Ile Ser Gly Asn
660 665 670

Arg Pro Ile Gly Ser Ile Ser Asp His Leu His Tyr Phe Val Ser Asn
675 680 685

Ile Glu Ala Asn Ala Gly Asp Asn Lys Leu Ser Lys Asn Ala Lys Glu
690 695 700

Asn Asn Ile Phe Glu Asn Leu Asn Tyr Asp Tyr Ile Gly Val Val Asn
705 710 715 720

Gly Asn Asn Thr Glu Glu Leu Phe Lys Val Leu Asn Asn Ile Lys Glu
725 730 735

Asn Lys Leu Lys Arg Ala Thr Val Leu His Val Arg Thr Lys Lys Ser
740 745 750

Asn Asp Phe Ile Asn Ser Lys Ser Pro Ile Ser Ile Leu His Ser Ile
755 760 765

Lys Lys Asn Glu Ile Phe Pro Phe Asp Thr Thr Ile Leu Asn Gly Asn
775 780

Ile His Lys Glu Asn Lys Ile Glu Glu Glu Lys Asn Val Ser Ser Ser
785 790 795 800

Thr Lys Tyr Asp Val Asn Asn Lys Asn Asn Lys Asn Asn Asp Asn Ser
 805 810 815

 Glu Ile Ile Lys Tyr Glu Asp Met Phe Ser Lys Glu Thr Phe Thr Asp
 820 825 830

 Ile Tyr Thr Asn Glu Met Ile Lys Tyr Leu Lys Lys Asp Arg Asn Ile
 835 840 845

 Ile Phe Leu Ser Pro Ala Met Leu Gly Gly Ser Gly Leu Val Lys Ile
 850 855 860

 Ser Glu Arg Tyr Pro Asn Asn Val Tyr Asp Val Gly Ile Ala Glu Gln
 865 870 875 880

 His Ser Val Thr Phe Ala Ala Ala Met Ala Met Asn Lys Lys Leu Lys
 885 890 895

 Ile Glu Leu Cys Ile Tyr Ser Thr Phe Leu Gln Arg Ala Tyr Asp Gln
 900 905 910

 Ile Ile His Asp Leu Asn Ile Gln Asn Ile Pro Leu Lys Val Ile Ile
 915 920 925

 Gly Arg Ser Gly Leu Val Gly Glu Asp Gly Ala Thr His Gln Gly Ile
 930 935 940

 Tyr Asp Leu Ser Tyr Leu Gly Thr Leu Asn Asn Ala Tyr Ile Ile Ser
 945 950 955 960

 Pro Ser Asn Gln Val Asp Leu Lys Arg Ala Leu Arg Phe Ala Tyr Leu
 965 970 975

 Asp Lys Asp His Ser Val Tyr Ile Arg Ile Pro Arg Met Asn Ile Leu
 980 985 990

 Ser Asp Lys Tyr Met Lys Gly Tyr Leu Asn Ile His Met Lys Asn Glu
 995 1000 1005

 Ser Lys Asn Ile Asp Val Asn Val Asp Ile Asn Asp Asp Val Asp Lys
 1010 1015 1020

 Tyr Ser Glu Glu Tyr Met Asp Asp Asp Asn Phe Ile Lys Ser Phe Ile
 1025 1030 1035 1040

 Gly Lys Ser Arg Ile Ile Lys Met Asp Asn Glu Asn Asn Asn Thr Asn
 1045 1050 1055

Glu His Tyr Ser Ser Arg Gly Asp Thr Gln Thr Lys Lys Lys Lys Val
1060 1065 1070

Cys Ile Phe Asn Met Gly Ser Met Leu Phe Asn Val Ile Asn Ala Ile
1075 1080 1085

Lys Glu Ile Glu Lys Glu Gln Tyr Ile Ser His Asn Tyr Ser Phe Ser
1090 1095 1100

Ile Val Asp Met Ile Phe Leu Asn Pro Leu Asp Lys Asn Met Ile Asp
1095 1110 1115 1120

His Val Ile Lys Gln Asn Lys His Gln Tyr Leu Ile Thr Tyr Glu Asp
1125 1130 1135

Asn Thr Ile Gly Gly Phe Ser Thr His Phe Asn Asn Tyr Leu Ile Glu
1140 1145 1150

Asn Asn Tyr Ile Thr Lys His Asn Leu Tyr Val His Asn Ile Tyr Leu
1155 1160 1165

Ser Asn Glu Pro Ile Glu His Ala Ser Phe Lys Asp Gln Gln Glu Val
1170 1175 1180

Val Lys Met Asp Lys Cys Ser Leu Val Asn Arg Ile Lys Asn Tyr Leu
1185 1190 1195 1200

Lys Asn Asn Pro Thr
1205